

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY

Searcher: P. Schweitzer

Searcher Phone #: 308-4272

Searcher Location: SM 12E18

Date Searcher Picked Up: 9/24

Date Completed: 9/24

Searcher Prep & Review Time: 5

Clerical Prep Time: _____

Online Time: 20

Type of Search

NA Sequence (#) 2

AA Sequence (#) _____

Structure (#) _____

Bibliographic _____

Litigation _____

Fulltext _____

Patent Family _____

Other _____

Vendors and cost where applicable

STN _____

Dialog _____

Questel/Orbit _____

Dr. Link _____

Lexis/Nexis _____

Sequence Systems GCG FastPB Ig FastPB

WWW/Internet _____

Other (specify) _____

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From: Portner, Ginny
Sent: Friday, September 21, 2001 11:16 AM
To: STIC-Biotech/ChemLib
Subject: FW: 09/252,691

actually, I don't need the sequence searched against the entire data base but only need SEQ ID NO 1394 searched against the following sequences. Thanks

-----]
ID PSI_RSU; PATTERN.
AC PS01149;
DT NOV-1995 (CREATED); JUL-1999 (DATA UPDATE); JUL-1999 (INFO UPDATE).
DE Rsu family of pseudouridine synthase signature.
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DR O51155, Y129_BORBU, T; Q55578, Y361_SYNY3, T; O66829, Y554_AQUAE, T;
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DR O05668, YRSU_MYCLE, T; O33210, YRSU_MYCTU, T; O32068, YTZF_BACSU, T;
DO PDOC00885;

Thanks

Original Message-----

Fr m: Portner, Ginny
//
Sent: Friday, September 21, 2001 11:05 AM
T : STIC-Biotech/ChemLib
Subject: 09/252,691

Please search SEQ ID No 1394.

Ginny Portner
CM1, Art Unit 1645
Room 7e13
Mail box 7e12
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CTFE

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The list of best scores is:

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KEYWORDS
SOURCE      Escherichia coli K12 BHB2600.
ORGANISM    Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
            Escherichia.
REFERENCE   1 (bases 1 to 39149)
AUTHORS    Richterich,P., Lakey,N., Gryan,G., Jaehn,L., Mintz,L., Robison,K.
            and Church,G.M.
TITLE      Automated multiplex sequencing of the E.coli genome
JOURNAL    Unpublished
REFERENCE   2 (bases 1 to 39149)
AUTHORS    Robison,K.
TITLE      Direct Submission
JOURNAL    Submitted (29-SEP-1993) Department of Genetics, Harvard Medical
            School, 200 Longwood Avenue, Boston MA 02115
REFERENCE   3 (bases 1 to 39149)
AUTHORS    Robison,K.
TITLE      Direct Submission
JOURNAL    Submitted (10-FEB-1994) Department of Genetics, Harvard Medical
            School, 200 Longwood Avenue, Boston MA 02115
COMMENT    On Feb 10, 1994 this sequence version replaced gi:405903.
            From E.coli K12 BHB2600. All of the sequence in this contig was
            sequenced at least twice on one strand and once on the other
            strand, except in the 2 regions marked. The annotation of this
            sequence should be considered preliminary and incomplete. Please
            contact KRobison@nucleus.harvard.edu before citing this sequence
            in a published work.
            Region: Centisome 49.
FEATURES
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               /db_xref="taxon:562"
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 outside ABC-family signatures."
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TITLE The complete genome sequence of the gram-positive bacterium

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AUTHORS
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FEATURES

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CDS

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terminator
gene
CDS

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CDS

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terminator

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CDS

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CDS

gene

terminator

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gene

CDS

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complement(21155. .21877)
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VSLTPKVELLYFLAKTPDKVYDREKLLKQVMEYFFGDLRTVTHVKRLREKLNKVS
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GYERFNVWDSKEKSVYTEMFALVPGHOGELLTEGRMEPLVDLPALFSGKRVNTVI
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FLRRGLFSTVTVLNGESKEKIVTLKKHXYIRKEGSILAEKFRSGRWGPIYVNH
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KVFADALRDGGRVAKNFQTDALVYKREGKIYVGEKPLEKTEEDIRVNPFRDS
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(penicillin-binding protein 5*)
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KIKLDVYGLMRSGNDAVAIAEHVGGSLDGFVYMMNOKAEOLGKMKNTFQNPGLDD
HENHYSTAYDMAILTKYAKLADYOKISCTKIYKAFTMESVYKKNKLLTMLYPYSTG
GKTYTKLAKFTLVSTASKDGLIATVINDNDNDHMKMFYFEHYQTVLIARKG
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CDS
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EREIEERRKKSRO"
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FLWKEDEIDVGAIGVEKKDSEVIRHISVNPSHRQHGIGKQMDALKHLFKTQVLVPN
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3,4-dihydroxy-2-butanone 4-phosphate synthase"
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CEIMNEDGTMARVPDELIEIAKKHOLKMITIKDLQYRYNLTLVREVIDITLPTDFT
EKVYGYTNEVDGKEHVAFMGDVPGPEEPVLRVHSECLTGDVFGSHRCDGCPQLHAA
LNQIAAEGRGVLLYLRLBQEGIGLNLKAKYKLEQGVITVEANRGAIGFLPDLRNTGI
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/db_xref="SWISS-PROT:P16440"
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GICLTVTDTKNOFTVDVMTKATSLNDLTGSKVNLERAMAANGRFGHFVSGHV
DGTAEITRIEKSNAVYDLKMDPSLTLYLVKGSITVDGYSLTIFGLTEDVTIISLI
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YGEAAEYHAIHMAGAAEGADIVVTLEPCSHYKTPPCAEIITNSGIRKRVFAMRDP
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ATSGDSKWTISEAARQAOQYRFTTHQSIILVGVTVKADNPSTLCRLPNVTQKQPVRI
LDTVLISPEDAKVICDQIAPTWTFTARADEKKKRLSAFGVNIITLTERIQIIPDVL
KILAEIGMSVYVEGGSVHGSFYKGCQEILFIYFAPKLIGGTHAPSLISGEGFSQM
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(stage V sporulation)"
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LRRIRDERLRVKRKRSKSDLSICYIEDADPOLVEIVEKEIASIDVDGLTMAD
KTYBEFTVQNSYFPFLVRYTERPDVAANHVLGHVLIIVDTSPIIITPTTFHHVQ
HAEYRQPSGVGFLVWRFEGILASTFLFPIWFLVLOPDLPPNNKFKIGLNKTHYI
PIIQLADLIGIEFLMAAHTHTALSTALSTAMGLIAVLIGQIAEVLGFLSEVILYVS
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STRSGAEVLKLIASADPYVPMFDDSLQAGEGEAALYVATHPSIEVLGVIAVAS
KTHQAEVYDVSDIRNGEITEYGVKVGEREFDHHRMSGDTVYCLDKLDLPLTIGIG
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ATSVYTCSGAVISQTPGDIQITSATYVKVSDLGITPFDMSGAMAPAAADTIKQHEK
DLNRTADDYDLILGLSGVSPVKDLKEDGYPVGTKKDDCCGLLIYTPDQQVAGG
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GGAS"
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complement(47398..48165)
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complement(47398..48165)
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/function="early forespore-specific gene expression"
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/product="RNA polymerase sporulation-specific sigma factor
(sigma-F)"
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PSSITHETVENDGDPITLLDQIADNSBEKFDKALKEAISDEEREKLIYLVRYKD
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complement(48177..48617)
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complement(48177..48617)
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ATP before septation; phosphorylation of SpoIIAA (stage II
sporulation)"
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serine kinase"
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complement(48614..48967)
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selectively in the forespore (stage II sporulation)"
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complement(49063..50232)
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GMDIAHAITAYNGFSIKTDVEFLNGLLNRGGIVGMLDSLVIIIFGLFGGLLEKLVG
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    RYPLVKVILPALVQGENASRIVTRIEANEKEICDVLVGRGGSGIEELNAFNEE
    IVARFASNPITISAVGHETDITSDVADIRATPTGAAGIAPVPTDILLERTKTA
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```


REFERENCE
AUTHORS

1 (bases 1 to 10959)
Blattner,F.R., Plunkett,G. III, Bloch,C.A., Perna,N.T., Burland,V.,
Riley,M., Collado-Vides,J., Glasner,J.D., Rode,C.K., Mayhew,G.F.,
Gregor,J., Davis,N.W., Kirkpatrick,H.A., Goeden,M.A., Rose,D.J.,
Mau,B. and Shao,Y.

TITLE
JOURNAL
MEDLINE
PUBMED

The complete genome sequence of *Escherichia coli* K-12
Science 277 (5331), 1453-1474 (1997)
97426617

REFERENCE
AUTHORS
TITLE
JOURNAL

2 (bases 1 to 10959)
Blattner,F.R.
Direct Submission
Submitted (16-JAN-1997) Guy Plunkett III, Laboratory of Genetics,
University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecollegenetics.wisc.edu Phone: 608-262-2534 Fax:
608-263-7459

REFERENCE
AUTHORS
TITLE
JOURNAL

3 (bases 1 to 10959)
Blattner,F.R.
Direct Submission
Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics,
University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecollegenetics.wisc.edu Phone: 608-262-2534 Fax:
608-263-7459

REFERENCE
AUTHORS
TITLE
JOURNAL

4 (bases 1 to 10959)
Plunkett,G. III
Direct Submission
Submitted (13-OCT-1998) Laboratory of Genetics, University of
Wisconsin, 445 Henry Mall, Madison, WI 53706, USA

COMMENT

This sequence was determined by the E. coli Genome Project at the
University of Wisconsin-Madison (Frederick R. Blattner director).
Supported by NIH grants HC00301 and HG01428 (from the Human Genome
Project and NCHGR). The entire sequence was independently
determined from E. coli K12 strain MG1655. Predicted open reading
frames were determined using GeneMark software, kindly supplied by
Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA,
30332 [e-mail: mark@amber.gatech.edu]. Open reading frames that
have been correlated with genetic loci are being annotated with CG
Site Nos., unique ID nos. for the genes in the E. coli Genetic
Stock center (CGSC) database at Yale University, kindly supplied by
Mary Berlyn. A public version of the database is accessible
(http://cgsc.biology.yale.edu). Annotation of the genome is an
ongoing task whose goal is to make the genome sequence more useful
by correlating it with other data. Comments to the authors are
appreciated. Updated information will be available at the E. coli
Genome Project's World Wide Web site
(http://www.genetics.wisc.edu). *** The E. coli K12 sequence and
its annotations are periodically updated; this is version M54. No
sequence changes. Annotation updates: updated gene identifications
and products; all new functional assignments courtesy of Monica
Riley; added promoters, protein binding sites, and repeated
sequences described in reference 1. The unique numeric identifiers
beginning with a lowercase 'b' assigned to each gene (protein- or
RNA-encoding) are now designated as gene synonyms instead of
labels. This should allow them to be searched for in Entrez as gene
names.

FEATURES
source

Location/Qualifiers
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COMMENT

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Group:

The Japan E.coli genome DNA sequencing group

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Horluchi, T., Ikemoto, K., Inada, T., Isono, K., Isono, S.,

Itoh, T., Kanai, K., Kasai, H., Kashimoto, K., Kim, S.,

Kimura, S., Kitagawa, M., Kitakawa, M., Makino, K.,

Masuda, S., Miki, T., Mizobuchi, K., Mori, H., Motomura, K.,

Nakamura, Y., Nishimoto, H., Nishio, Y., Oshima, T., Saito, N.,

Sampel, G., Seki, Y., Tagami, H., Takemoto, K., Wada, C.,

Yamamoto, Y. and Yano, M.

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URL:

The Japan E. coli genome database

http:bsw3.aist-nara.ac.jp.

Location/Qualifiers

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Genome Project's World Wide Web site
(http://www.genetics.wisc.edu). *** The E. coli K12 sequence and
its annotations are periodically updated; this is version M54. No
sequence changes. Annotation updates: updated gene identifications
and products; all new functional assignments courtesy of Monica
Riley; added promoters, protein binding sites, and repeated
sequences described in reference 1. The unique numeric identifiers
beginning with a lowercase 'b' assigned to each gene (protein- or
RNA-encoding) are now designated as gene synonyms instead of
labels. This should allow them to be searched for in Entrez as gene
names.

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FEATURES
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DEFINITION Escherichia coli genomic DNA. (25.6 - 25.9 min).
ACCESSION D90748 AB001340
VERSION D90748.1 GI:1651553
KEYWORDS Complete and shotgun sequencing; potB; potA; potH; pepT; phoQ; phoP;
purB; ycfC; ycfB; icdA; icd; icdE; lit.
SOURCE Escherichia coli (strain:K12) DNA, clone:Kohara clone #239.
ORGANISM Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
REFERENCE
AUTHORS Oshima,T., Alba,H., Baba,T., Fujita,K., Hayashi,K., Honjo,A.,
Ikemoto,K., Inada,T., Itoh,T., Kajihara,M., Kanai,K., Kashimoto,K.,
Kimura,S., Kitagawa,M., Makino,K., Masuda,S., Miki,T.,
Mizobuchi,K., Mori,H., Motomura,K., Nakamura,Y., Nishio,Y.,
Nishio,Y., Saito,N., Sampei,G., Seki,Y., Tagami,H., Takemoto,K.,
Wada,C., Yamamoto,Y., Yano,M. and Horiuchi,T.
A 718-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 12.7-28.0 min region on the linkage map
DNA Res. 3 (3), 137-155 (1996)
2 (sites)
Alba,H., Baba,T., Fujita,K., Hayashi,K., Honjo,A., Horiuchi,T.,
Ikemoto,K., Inada,T., Isono,K., Isono,S., Itoh,T., Kanai,K.,
Kasai,H., Kashimoto,K., Kim,S., Kimura,S., Kitagawa,M.,
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Motomura,K., Nakamura,Y., Nishimoto,H., Nishio,Y., Oshima,T.,
Saito,N., Sampei,G., Seki,Y., Tagami,H., Takemoto,K., Wada,C.,
Yamamoto,Y. and Yano,M.
The systematic sequencing of the Escherichia coli genome in Japan
Unpublished (1996)
3 (bases 1 to 15007)
Mori,H.
Direct Submission
Submitted (29-JUL-1996) to the DDBJ/EMBL/GenBank databases.
Hirota Mori, NARA Institute of Science and Technology, Res. &
Edu. Center for Genetic Info.; 8916-5 Takayama, Ikoma, Nara 630-01,
Japan (E-mail:hmori@gtc.aist-nara.ac.jp, Tel:81-7437-2-5660,
Fax:81-7437-2-5669)
Collaboration information:
Project:
The Japan E.coli genome DNA sequencing project
Group:
The Japan E.coli genome DNA sequencing group
Members: (1995.4 - 1996.3)
Alba,H., Baba,T., Fujita,K., Hayashi,K., Honjo,A.,
Horiuchi,T., Ikemoto,K., Inada,T., Isono,K., Isono,S.,
Itoh,T., Kanai,K., Kasai,H., Kashimoto,K., Kim,S.,
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Masuda,S., Miki,T., Mizobuchi,K., Mori,H., Motomura,K.,
Nakamura,Y., Nishimoto,H., Nishio,Y., Oshima,T., Saito,N.,
Sampei,G., Seki,Y., Tagami,H., Takemoto,K., Wada,C.,
Yamamoto,Y. and Yano,M.

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URL:

The Japan E. coli genome database
http://bsw3.aist-nara.ac.jp.

FEATURES

source

Location/Qualifiers

1..15007

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/strain="K12"

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/clone="Kohara clone #239"

/map="25.6-25.9 min"

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AVNKRPLLLDLSALDYKLRKQKQNELKALQKRLGTFVFDHDEQALMSDRI

NYVRDRIQDGTPREIYEENKLVFAGFGEINMNFATVIRLDEQVRANVEGEC

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Members: (1995.4 - 1996.3)

Alba, H., Baba, T., Fujita, K., Hayashi, K., Honjo, A.,
Horiuchi, T., Ikemoto, K., Inada, T., Isono, K., Isono, S.,
Itoh, T., Kanai, K., Kasai, H., Kashimoto, K., Kim, S.,
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Masuda, S., Miki, T., Mizobuchi, K., Mori, H., Motomura, K.,
Nakamura, Y., Nashimoto, H., Nishio, Y., Oshima, T., Saito, N.,
Sampei, G., Seki, Y., Tagami, H., Takemoto, K., Wada, C.,
Yamanoto, Y. and Yano, M.

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URL:
http://bsw3.aist-nara.ac.jp

FEATURES
source

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CDS

CDS

CDS

CDS

CDS

CDS

CDS

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DEFINITION *Bacillus subtilis* complete genome (section 13 of 21): from 2395261 to 2613730.
ACCESSION Z99116 AL009126
VERSION Z99116.1 GI:2634723
KEYWORDS
SOURCE
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Bacteria: Firmicutes; *Bacillus*/Clostridium group; *Bacillus*.
REFERENCE 1 (bases 1 to 218470)
AUTHORS Kunst, F., Ogasawara, N., Moszer, I., Albertini, A.M., Alloni, G., Azevedo, V., Bertero, M.G., Bessieres, P., Bolotin, A., Borchert, S., Borriss, R., Boursier, L., Brans, A., Braun, M., Brignell, S.C., Bron, S., Brouillet, S., Bruschi, C.V., Caldwell, B., Capuano, V., Carter, N.M., Choi, S.K., Codani, J.J., Conner, I.F., Cummings, N.J., Daniel, R.A., Denizot, F., Devine, K.M., Dusterhoft, A., Ehrlich, S.D., Emerson, P.T., Entian, K.D., Errington, J., Fabret, C., Ferrari, E., Foulger, D., Fritz, C., Fujita, M., Fujita, Y., Fuma, S., Galizzi, A., Gallaron, N., Ghim, S.Y., Glaser, P., Goffeau, A., Gollightly, E.J., Grandi, G., Guiseppli, G., Guy, B.J., Haga, K., Halech, J., Harwood, C.R., Henaut, A., Hilbert, H., Holsappel, S., Hosono, S., Hullo, M.F., Itaya, M., Jones, L., Joris, B., Karamata, D., Kasahara, Y., Klier-Blanchard, M., Klein, C., Kobayashi, Y., Koetter, P., Konigstein, G., Krogh, S., Kumano, M., Kurita, K., Lapidus, A., Lardinois, S., Lauber, J., Lazarevic, V., Lee, S.M., Levine, A., Liu, H., Masuda, S., Maue, C., Medigue, C., Medina, N., Mellado, R.P., Mizuno, M., Moestl, D., Nakai, S., Noback, M., Noone, D., O'Reilly, M., Ogawa, K., Ogihara, A., Oudega, B., Park, S.H., Parro, V., Pohl, T.M., Portetelle, D., Portwollik, S., Prescott, A.M., Presecan, E., Pujic, P., Purnelle, B., Rapoport, G., Rey, M., Reynolds, S., Rieger, M., Rivolta, C., Rocha, E., Roche, B., Rose, M., Sadane, Y., Sato, T., Scanlan, E., Schleich, S., Schroeter, R., Scoffone, F., Sekiguchi, J., Sekowska, A., Seror, S.J., Serror, P., Shin, B.S., Soldo, B., Sorokin, A., Tacconi, E., Takagi, T., Takahashi, H., Takemaru, K., Takeuchi, M., Tamakoshi, A., Tanaka, T., Terpstra, P., Tognoni, A., Tosato, V., Uchiyama, S., Vandenbol, M., Vannier, F., Vassarotti, A., Viari, A., Wambutt, R., Wedler, E., Wedler, H., Weitzenecker, T., Winters, P., Wipat, A., Yamamoto, H., Yamane, K., Yasumoto, K., Yata, K., Yoshida, K., Yoshikawa, H.F., Zumstein, E., Yoshikawa, H. and Danchin, A.

TITLE The complete genome sequence of the gram-positive bacterium *Bacillus subtilis*
JOURNAL Nature 390 (6657), 249-256 (1997)
MEDLINE 98044033
REFERENCE 2 (bases 1 to 218470)
AUTHORS Kunst, F., Ogasawara, N., Yoshikawa, H. and Danchin, A.
TITLE Direct Submission
JOURNAL Submitted (18-NOV-1997) I. Moszer, A. Danchin, Institut Pasteur, Regulation de l'Expression Genetique, 28 rue du Docteur Roux, 75724 Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.fr.
adanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41, Fax: +33 (0)1 45 68 89 48

FEATURES
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44746..45762
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47398..48165
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DGTHTVYSKRELGNKIRAKDELSKTIGRVPVQEIADHLEIEAEDVYLAQEVRA
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48177..48617
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/notes="mutants lead to the production of immature spores
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ATP before septation; phosphorylation of SpoIIAA (stage II
sporulation)"
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serine kinase"
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selectively in the forespore (stage II sporulation)"
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binding protein)"
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ribose-5-P/deoxyribose-5-P (purine nucleoside salvage)"
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LQAAHEVVVPLEELRYICARELTLDPKYMGRIIARFVGPFGQFKRPNRHDYA
LKPFDRTVMNELKDCGLDVISIGKSIDYDEGITSRRVTSNMNMDKVIDTIGEDF
TGLSFANLVDFDALGHRHRRPEGYGRALEEFDAFLPEVFGKMRREDLLIITADHNDP
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ROCFWKNLKIATLEAGIKKELTPTLHRSFATHLEDAADLRAVQEMGLHADISTTOI
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CDS	

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CDS

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CDS

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terminator

gene

CDS

gene

CDS

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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Direct Submission
Submitted (29-SEP-1993) Department of Genetics, Harvard Medical School, 200 Longwood Avenue, Boston MA 02115
3 (bases 1 to 39149)
Robison, K.
Direct Submission
Submitted (10-FEB-1994) Department of Genetics, Harvard Medical School, 200 Longwood Avenue, Boston MA 02115
On Feb 10, 1994 this sequence version replaced gi:405903.
From E.coli K12 BHB2600. All of the sequence in this contig was sequenced at least twice on one strand and once on the other strand, except in the 2 regions marked. The annotation of this sequence should be considered preliminary and incomplete. Please contact KRobison@nucleus.harvard.edu before citing this sequence in a published work.
Region: Centisome 49.

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1487..2326
/gene="yejC -- probably a frameshift fragment of yejB"
2326..3351
/gene="probable transport operon; yejA-yejB/C-yejE-yejF.
Homologous to ABC-type transporters; closest similarity to oligopeptide transporters. Close proximity of inferred start and stop codons suggests translational coupling between all 4 genes."
/note="Probable membrane-bound component of transport complex"

CDS
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3353..4942
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Homologous to ABC-type transporters; closest similarity to oligopeptide transporters. Close proximity of inferred start and stop codons suggests translational coupling between all 4 genes."
/note="ABC-type ATP-dependent transport protein, perhaps of oligopeptides"
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complement(24709..25311)
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Alcaligenes eutrophus; weak match to Human guanylate
cyclase"
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WEILTVSLV"
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NPVSLMRGLVMGSGALLILALFLDLVVEHGWGHCIPCVGLVGSGLVITY
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/protein_id="AA16397.1"
/db_xref="GI:405930"
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KVLPLSLARGEIGHYHFRFGLWEGNNGKS"
complement(26839..27312)
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several proteins with redox functions"
/codon_start=1
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CDS	EDIPCAKCVSPGSGALDRIEISIDDARMGLAVLVQENCLNFQGPALRCLLSRMPEN" complement(27319..29748) /note="may be part of aeg-46.5 operon; strong match to the periplasmic nitrate reductase large subunit (napA) from Alcaligenes eutrophus; GTG start codon" /codon_start=1 /transl_table=11 /product="yojC" /protein_id="AAAL16399.1" /db_xref="GI:453989"	CDS	complement(32159..33631) /codon_start=1 /transl_table=11 /product="yojH" /protein_id="AAAL16402.1" /db_xref="GI:424051"
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CDS	IVVEAEDSETLIQTIESVFNVEGVSLVSLVYHQEQGEETP" complement(30054..30548) /note="probable ferredoxin or Fe-S protein; probably part of aeg-46.5 operon" /codon_start=1 /transl_table=11 /product="yojG" /protein_id="AAAL16401.1" /db_xref="GI:453990"	CDS	/note="DNA repair protein" /codon_start=1 /transl_table=11 /product="yojK" /protein_id="AAAL16404.1" /db_xref="GI:405940"
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repeat_region	KGMKROVIQTPQEDSTLAVELLIGOTLEDCNHLGCKLENKTLGEGYDYVFD EKIDNAVVR" 31533..31654 /rpt_family="REP/PU"	misc_feature	36978..37132 /note="CAUTION! Low coverage in this region of the sequence"
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repeat_region	31814..31845 /rpt_family="REP/PU"		
repeat_region	31875..31981 /rpt_family="REP/PU"		
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BASE COUNT 9381 a 10833 c 9785 g 9150 t
ORIGIN

000008 Length: 39149 September 24, 2001 09:20 Type: N Check: 8999
Initial Score = 78 Optimized Score = 291 Significance = -0.78
Residue Identity = 49% Matches = 358 Mismatches = 275
Gaps = 95 Conservative Substitutions = 0

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13350 13360 13370 13380 13390 X 13400 13410
20
TAACATC--CCGCC-----ATTCCCGTTGCGCAGGATCAGCGTATAGTGCCTAGCGGTAGCAATA
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ACATCATCAGCGCTGTTTATTCTTG--TTATCAAGACGTCCAGCACACCCGCC--TG-AGTATCCA--C
13420 13430 13440 13450 13460 13470
90
GTCGAGGTAGGGAAGCCACATCGCCAGTCAT--GC-GCCTGAC--CTG--TCGGTTCGGCCCTTATATAAG
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160
GGTGATTTTAAAGCCAG-CTGCTA---GGAA-TGGATTTACCTCAGCAATCGCGGGTTCG--CCGGC---C
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GATGACCTTATACAGCCTGATAACGCCACTGTCAGCCACATCATTTATTAATTTGCCATCGTCATTA
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13620 13630 13640 13650 13660 13670 13680
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CGTTGCGCAGCTTTGCCA--CGGA--CGCGT--CGTCCGCTCGCCTTCAACCTGCACATA--GTAAATTTTTCG
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13690 13700 13710 13720 13730 13740 13750
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13890 13900 13910 13920 13930 13940 13950
560
TGGGGT--TCGGC-GTCTTCTCGTGGCTTGTG--GTGAGCTGAATCGCTCAACCGGTTGTTTCTTAAAG-
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13960 13970 13980 13990 14000 14010 14020
630
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7. US-09-252-691C-1394' (1-669)
109228 TOIG Of: 109228 check: 8816 from: 1 to: 28206

TOIG of: 109228 check: 8816 from: 1 to: 28206

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LOCUS      BACDIA      28206 bp      DNA      BCT      26-MAY-1995
DEFINITION Bacillus subtilis spoVA to serA region.
ACCESSION  L09228
VERSION    L09228.1 GI:410114
KEYWORDS   3-dehydroquinate dehydratase; aroC gene; diaminopimelate
            decarboxylase; lysA gene; penicillin-binding protein;
            peptidyl-prolyl isomerase; phosphoglycerate dehydrogenase; ppIB
            gene; response regulator; response regulator kinase; ribA gene;
            ribB gene; ribD gene; ribG gene; ribH gene; ribT gene; riboflavin
            biosynthesis operon; serA gene; signal peptidase; sipS gene; spoA
            gene; spoVAF gene.
SOURCE     Bacillus subtilis (strain 168, sub_species Marburg) DNA.
ORGANISM   Bacillus subtilis
            Bacteria; Firmicutes; Bacillus/Clostridium group;
            Bacillus/Staphylococcus group; Bacillus.
REFERENCE  1 (bases 1 to 28206)
            Yamamoto,J., Shimizu,M. and Yamane,K.
            Molecular cloning and analysis of nucleotide sequence of the
            Bacillus subtilis lysA gene region using B. subtilis phage vectors
            and a multi-copy plasmid, pUB110
            Agric. Biol. Chem. 55 (6), 1615-1626 (1991)
JOURNAL    91345841
MEDLINE    91345841
REFERENCE  2 (bases 1 to 28206)
            Buchanan,C.E. and Ling,M.L.
            Isolation and sequence analysis of dacB, which encodes a
            sporulation-specific penicillin-binding protein in Bacillus
            subtilis
            J. Bacteriol. 174 (6), 1717-1725 (1992)
JOURNAL    92193254
MEDLINE    92193254
REFERENCE  3 (bases 1 to 28206)
            Sorokin,A., Zumstein,E., Azevedo,V., Ehrlich,S.D. and Serror,P.
            The organization of the Bacillus subtilis 168 chromosome region
            between the spoVA and serA genetic loci, based on sequence data
            Mol. Microbiol. 10 (2), 385-395 (1993)
JOURNAL    95020538
MEDLINE    95020538
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RPDVAANHVLGHHVLIIVDTPSPVLIPTTLFHHVQHAERYRQAPSVGTFLRWRFRFG
ILASTLPLFWLFWLQPDGLGPNMKRFGKNDKTHIPILIIQIFLADLGIEFLRMAAIIH
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